

SEQUENCE LISTING

<110> Johansen, Teit E.

Blom, Nikolaj

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<120> Novel Neurotrophic Factors

<130> 19313-001 DIV

<140> U.S.S.N 09/662,183

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<150> DANISH 1998 00904

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<150> DANISH 1998 01265

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<150> 09/347,613

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<160> 76

<170> PatentIn Ver. 2.1

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<222> (1)..(119)

<220>

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<222> (721)..(865)

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<222> (120)..(179)

<220>

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<222> (405)..(719)

<220>

<221> misc_structure

<222> (661)..(663)

<223> CARBOHYD: Glycosylated Asparagine at Asn87

<220>

<221> misc_structure

<222> (426)..(623)

<223> DISULFID - Cys8-Cys73 disulfide bridge

<220>

<221> misc_structure

<222> (507)..(707)

<223> DISULFID: Cys35-Cys101 disulfide bridge

<220>

<221> misc_structure

<222> (519)..(713)

<223> DISULFID: Cys39-Cys103 disulfide bridge

<220>

<221> misc_structure

<222> (616)..(619)

<223> DISULFID: Cys72-Cys72 interchain disulfide bridge

<400> 1

ctaggagccc atgcccgcc tgatctcagc ccgaggacag cccctccttg aggtccttcc 60

tccccaagcc cacctgggtg ccccttttct ccctgaggct ccacttggtc tctccgcgc 119

atg cct gcc ctg tgg ccc acc ctg gcc gct ctg gct ctg ctg agc agc 167
Met Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala Leu Leu Ser Ser
-95 -90 -85 -80

gtc gca gag gcc tcc ctg ggc tcc gcg ccc cgc agc cct gcc ccc cgc 215
Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser Pro Ala Pro Arg
-75 -70 -65

gaa ggc ccc ccg cct gtc ctg gcg tcc ccc gcc ggc cac ctg ccg ggg 263
Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly His Leu Pro Gly
-60 -55 -50

gga cgc acg gcc cgc tgg tgc agt gga aga gcc cgg cgg ccg cgc cgc 311
Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg Pro Arg Arg
-45 -40 -35

aga cac ttc tcg gcc cgc gcc ccc gcc gcc tgc acc ccc atc tgc tct 359
Arg His Phe Ser Ala Arg Ala Pro Ala Ala Cys Thr Pro Ile Cys Ser
-30 -25 -20

tcc ccg cgg gtc cgc gcg gcg cgg ctg ggg ggc cgg gca gcg cgc tcg 407
Ser Pro Arg Val Arg Ala Ala Arg Leu Gly Gly Arg Ala Ala Arg Ser
-15 -10 -5 -1 1

ggc agc ggg ggc gcg ggg tgc cgc ctg cgc tcg cag ctg gtg ccg gtg 455
Gly Ser Gly Gly Ala Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val
5 10 15

cgc gcg ctc ggc ctg ggc cac cgc tcc gac gag ctg gtg cgt ttc cgc 503
Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg
20 25 30

ttc tgc acc ggc tcc tgc ccg cgc gcg cgc tct cca cac gac ctc agc 551
Phe Cys Thr Gly Ser Cys Pro Arg Ala Arg Ser Pro His Asp Leu Ser
35 40 45

ctg gcc agc cta ctg ggc gcc ggg gcc ctg cga ccg ccc ccg ggc tcc 599
Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser
50 55 60 65

cgg ccc gtc agc cag ccc tgc tgc cga ccc acg cgc tac gaa gcg gtc 647
Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val

70 75 80

tcc ttc atg gac gtc aac agc acc tgg aga acc gtg gac cgc ctc tcc 695
Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser
85 90 95

gcc acc gcc tgc ggc tgc ctg ggc tgagggtctg ctccagggt ttgcagactg 749
Ala Thr Ala Cys Gly Cys Leu Gly
100 105

gaccttacc ggtggctctt cctgcctggg accctcccgc agagtccac tagccagcgg 809

cctcagccag ggacgaaggc ctcaaagctg agaggcccct gccggtgggt gatgga 865

<210> 2

<211> 200

<212> PRT

<213> Homo sapiens

<400> 2

Met Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala Leu Ser Ser
-95 -90 -85 -80

Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser Pro Ala Pro Arg
-75 -70 -65

Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly His Leu Pro Gly
-60 -55 -50

Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg Pro Arg Arg
-45 -40 -35

Arg His Phe Ser Ala Arg Ala Pro Ala Ala Cys Thr Pro Ile Cys Ser
-30 -25 -20

Ser Pro Arg Val Arg Ala Ala Arg Leu Gly Gly Arg Ala Ala Arg Ser
-15 -10 -5 -1 1

Gly Ser Gly Gly Ala Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val
5 10 15

Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg
20 25 30

Phe Cys Thr Gly Ser Cys Pro Arg Ala Arg Ser Pro His Asp Leu Ser

<221> mat_peptide

<222> (379)..(717)

<220>

<221> misc_structure

<222> (661)..(663)

<223> CARBOHYD: glycosylated Asparagine as Asn122

<220>

<221> misc_structure

<222> (424)..(621)

<223> DISULFID: Cys43-Cys108 disulfide bridge

<220>

<221> misc_structure

<222> (505)..(705)

<223> DISULFID: Cys70-Cys136 disulfide bridge

<220>

<221> misc_structure

<222> (517)..(711)

<223> DISULFID: Cys74-Cys138 disulfide bridge

<220>

<221> misc_structure

<222> (616)..(618)

<223> DISULFID: Cys107-Cys107 interchain disulfide
bridge

<400> 3

gagccc atg ccc ggc ctg atc tca gcc cga gga cag ccc ctc ctt gag 48

Met Pro Gly Leu Ile Ser Ala Arg Gly Gln Pro Leu Leu Glu

-95 -90 -85

gtc ctt cct ccc caa gcc cac ctg ggt gcc ctc ttt ctc cct gag gct 96

Val Leu Pro Pro Gln Ala His Leu Gly Ala Leu Phe Leu Pro Glu Ala

-80 -75 -70

cca ctt ggt ctc tcc gcg cag cct gcc ctg tgg ccc acc ctg gcc gct 144

Pro Leu Gly Leu Ser Ala Gln Pro Ala Leu Trp Pro Thr Leu Ala Ala

-65 -60 -55

ctg gct ctg ctg agc agc gtc gca gag gcc tcc ctg ggc tcc gcg ccc 192

Leu Ala Leu Leu Ser Ser Val Ala Glu Ala Ser Leu Gly Ser Ala Pro

-50 -45 -40

cgc agc cct gcc ccc cgc gaa ggc ccc ccg cct gtc ctg gcg tcc ccc 240
Arg Ser Pro Ala Pro Arg Glu Gly Pro Pro Pro Val Leu Ala Ser Pro
-35 -30 -25 -20

gcc ggc cac ctg ccg ggg gga cgc acg gcc cgc tgg tgc agt gga aga 288
Ala Gly His Leu Pro Gly Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg
-15 -10 -5

gcc cgg cgg ccg ccg ccg cag cct tct cgg ccc gcg ccc ccg ccg cct 336
Ala Arg Arg Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Pro
-1 1 5 10

gca ccc cca tct gct ctt ccc cgc ggg ggc cgc gcg gcg cgg gct ggg 384
Ala Pro Pro Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly
15 20 25

ggc ccg ggc aac cgc gct cgg gca gcg ggg gcg cgg ggc tgc cgc ctg 432
Gly Pro Gly Asn Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu
30 35 40 45

cgc tcg cag ctg gtg ccg gtg cgc gcg ctc ggc ctg ggc cac cgc tcc 480
Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser
50 55 60

gac gag ctg gtg cgt ttc cgc ttc tgc agc ggc tcc tgc cgc cgc gcg 528
Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala
65 70 75

cgc tct cca cac gac ctc agc ctg gcc agc cta ctg ggc gcc ggg gcc 576
Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala
80 85 90

ctg cga ccg ccc ccg ggc tcc ccg ccc gtc agc cag ccc tgc tgc cga 624
Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg
95 100 105

ccc acg cgc tac gaa gcg gtc tcc ttc atg gac gtc aac agc acc tgg 672
Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp
110 115 120 125

aga acc gtg gac cgc ctc tcc gcc aac ccc tgc ggc tgc ctg ggc 717
Arg Thr Val Asp Arg Leu Ser Ala Asn Pro Cys Gly Cys Leu Gly
130 135 140

tgagggctcg ctccagggtc ttgcagactg gacccttacc ggtggctctt cctgcctggg 777

accctccgc agagtccac tagccagcgg cctcagccag ggacgaaggc ctcaaagctg 837

agaggccct gccggtgggt gatg 861

<210> 4

<211> 237

<212> PRT

<213> Homo sapiens

<400> 4

Met Pro Gly Leu Ile Ser Ala Arg Gly Gln Pro Leu Leu Glu Val Leu
-95 -90 -85

Pro Pro Gln Ala His Leu Gly Ala Leu Phe Leu Pro Glu Ala Pro Leu
-80 -75 -70

Gly Leu Ser Ala Gln Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala
-65 -60 -55 -50

Leu Leu Ser Ser Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser
-45 -40 -35

Pro Ala Pro Arg Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly
-30 -25 -20

His Leu Pro Gly Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg
-15 -10 -5

Arg Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Ala Pro
-1 1 5 10 15

Pro Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly Gly Pro
20 25 30

Gly Asn Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser
35 40 45

Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu
50 55 60

Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser
65 70 75

Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg
80 85 90 95

Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr
100 105 110

Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr
115 120 125

Val Asp Arg Leu Ser Ala Asn Pro Cys Gly Cys Leu Gly
130 135 140

<210> 5

<211> 140

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (134)

<223> Wherein Xaa at position 134 designates Asn or Thr

<220>

<221> VARIANT

<222> (135)

<223> Wherein Xaa at position 135 designates Ala or Pro

<400> 5

Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Ala Pro Pro
1 5 10 15

Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly Gly Pro Gly
20 25 30

Asn Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln
35 40 45

Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu
50 55 60

Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro
65 70 75 80

His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro
85 90 95

Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg
100 105 110

Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val
115 120 125

Asp Arg Leu Ser Ala Xaa Xaa Cys Gly Cys Leu Gly
130 135 140

<210> 6

<211> 116

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (110)

<223> Wherein Xaa at position 110 designates Asn or Thr

<220>

<221> VARIANT

<222> (111)

<223> Wherein Xaa at position 111 designates Ala or Pro

<400> 6

Ala Ala Arg Ala Gly Gly Pro Gly Asn Arg Ala Arg Ala Ala Gly Ala
1 5 10 15

Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly
20 25 30

Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly
35 40 45

Ser Cys Arg Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu
50 55 60

Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser
65 70 75 80

Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp
85 90 95

Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Xaa Xaa Cys
100 105 110

Gly Cys Leu Gly
115

<210> 7

<211> 113

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (107)

<223> Wherein Xaa at position 107 designates Asn or Thr

<220>

<221> VARIANT

<222> (108)

<223> Wherein Xaa at position 108 designates Ala or Pro

<400> 7

Ala Gly Gly Pro Gly Asn Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys
1 5 10 15

Arg Leu Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly His
20 25 30

Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg
35 40 45

Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala
50 55 60

Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys
65 70 75 80

Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser
85 90 95

Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Xaa Xaa Cys Gly Cys Leu
100 105 110

Gly

<210> 8
<211> 861
<212> DNA
<213> Homo sapiens

<220>
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<220>
<221> 5'UTR
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<220>
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<222> (718)..(861)

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<222> (298)..(717)

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<222> (370)..(717)

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<221> mat_peptide
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<220>
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<222> (661)..(663)
<223> CARBOHYD: glycosylated asparagine at Asn122

<220>
<221> misc_structure
<222> (424)..(621)
<223> DISULFID: Gly43-Gly108 disulfide bridge

<220>
<221> misc_structure
<222> (505)..(705)

<223> DISULFID: Gly70-Gly136 disulfide bridge

<220>

<221> misc_structure

<222> (517)..(711)

<223> DISULFID: Gly74-Gly138 disulfide bridge

<220>

<221> misc_structure

<222> (616)..(618)

<223> DISULFID: Gly107-Gly107 interchain disulfide
bridge

<400> 8

aggagggtgg gggaacagct caacaatggc tgatgggcgc tcctggtgtt gatagag 57

atg gaa ctt gga ctt gga ggc ctc tcc acg ctg tcc cac tgc ccc tgg 105
Met Glu Leu Gly Leu Gly Gly Leu Ser Thr Leu Ser His Cys Pro Trp
-80 -75 -70 -65

cct agg cgg cag cct gcc ctg tgg ccc acc ctg gcc gct ctg gct ctg 153
Pro Arg Arg Gln Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala Leu
-60 -55 -50

ctg agc agc gtc gca gag gcc tcc ctg ggc tcc gcg ccc cgc agc cct 201
Leu Ser Ser Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser Pro
-45 -40 -35

gcc ccc cgc gaa ggc ccc ccg cct gtc ctg gcg tcc ccc gcc ggc cac 249
Ala Pro Arg Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly His
-30 -25 -20

ctg ccg ggg gga cgc acg gcc cgc tgg tgc agt gga aga gcc cgg cgg 297
Leu Pro Gly Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg
-15 -10 -5 -1

ccg ccg ccg cag cct tct cgg ccc gcg ccc ccg ccg cct gca ccc cca 345
Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Pro Ala Pro Pro
1 5 10 15

tct gct ctt ccc cgc ggg ggc cgc gcg gcg cgg gct ggg ggc ccg ggc 393
Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly Gly Pro Gly
20 25 30

agc cgc gct cgg gca gcg ggg gcg cgg ggc tgc cgc ctg cgc tgc cag 441
Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln

35 40 45
 ctg gtg ccg gtg cgc gcg ctc ggc ctg ggc cac cgc tcc gac gag ctg 489
 Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu
 50 55 60

 gtg cgt ttc cgc ttc tgc agc ggc tcc tgc cgc cgc gcg cgc tct cca 537
 Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro
 65 70 75 80

 cac gac ctc agc ctg gcc agc cta ctg ggc gcc ggg gcc ctg cga ccg 585
 His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro
 85 90 95

 ccc ccg ggc tcc cgg ccc gtc agc cag ccc tgc tgc cga ccc acg cgc 633
 Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg
 100 105 110

 tac gaa gcg gtc tcc ttc atg gac gtc aac agc acc tgg aga acc gtg 681
 Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val
 115 120 125

 gac cgc ctc tcc gcc acc gcc tgc ggc tgc ctg ggc tgagggtcgc 727
 Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly
 130 135 140

 ctccagggtc ttgcagactg gacccttacc ggtggctctt cctgcctggg accctcccgc 787

 agagtcacac tagccagcgg cctcagccag ggacgaaggc ctcaaagctg agaggcccct 847

 accggtgggt gatg 861

 <210> 9
 <211> 220
 <212> PRT
 <213> Homo sapiens

 <400> 9
 Met Glu Leu Gly Leu Gly Gly Leu Ser Thr Leu Ser His Cys Pro Trp
 -80 -75 -70 -65

 Pro Arg Arg Gln Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala Leu
 -60 -55 -50

 Leu Ser Ser Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser Pro

-45 -40 -35
 Ala Pro Arg Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly His
 -30 -25 -20
 Leu Pro Gly Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg
 -15 -10 -5 -1
 Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Pro Ala Pro Pro
 1 5 10 15
 Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly Gly Pro Gly
 20 25 30
 Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln
 35 40 45
 Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu
 50 55 60
 Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro
 65 70 75 80
 His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro
 85 90 95
 Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg
 100 105 110
 Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val
 115 120 125
 Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly
 130 135 140

<210> 10
 <211> 140
 <212> PRT
 <213> Homo sapiens

 <220>
 <221> CARBOHYD
 <222> (122)
 <223> glycosylated asparagine

<400> 10

Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Ala Pro Pro
1 5 10 15

Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly Gly Pro Gly
20 25 30

Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln
35 40 45

Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu
50 55 60

Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro
65 70 75 80

His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro
85 90 95

Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg
100 105 110

Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val
115 120 125

Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly
130 135 140

<210> 11

<211> 116

<212> PRT

<213> Homo sapiens

<220>

<221> CARBOHYD

<222> (98)

<223> glycosylated asparagine

<400> 11

Ala Ala Arg Ala Gly Gly Pro Gly Ser Arg Ala Arg Ala Ala Gly Ala
1 5 10 15

Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly
20 25 30

Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly
35 40 45

Ser Cys Arg Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu
50 55 60

Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser
65 70 75 80

Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp
85 90 95

Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Thr Ala Cys
100 105 110

Gly Cys Leu Gly
115

<210> 12

<211> 113

<212> PRT

<213> Homo sapiens

<220>

<221> CARBOHYD

<222> (95)

<223> glycosylated asparagine

<400> 12

Ala Gly Gly Pro Gly Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys
1 5 10 15

Arg Leu Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly His
20 25 30

Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg
35 40 45

Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala
50 55 60

Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys
65 70 75 80

Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser
85 90 95

Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu
100 105 110

Gly

<210> 13
<211> 102
<212> DNA
<213> Homo sapiens

<400> 13
cctggccagc ctactgggcg ccggggccct gcgaccgcc ccgggctccc ggcccgtcag 60
ccagccctgc tgccgaccca cgcgctacga agcggctctc tt 102

<210> 14
<211> 220
<212> DNA
<213> Murinae gen. sp.

<400> 14
ggccaccgct ccgacgagct gatacgttc cgcttctgca ggggctcgtg ccgccgagca 60
cgctccagc acgatctcag tctggccagc ctactgggcg ctggggccct acggtcgcct 120
cccgggtccc ggccgatcag ccagccctgc tgccggccca ctgctatga ggccgtctcc 180
ttcatggacg tgaacagcac ctggagaacc gtggaccgcc 220

<210> 15
<211> 2136
<212> DNA
<213> Murinae gen. sp.

<220>
<221> CDS
<222> (975)..(1646)

<400> 15
gcgccgcgga attcggcacg agggcgcttc gctgcagccc gcgatctcta ctctgcctcc 60
tgggggtcttc tccaaatgtc tagccccac ctagaggggac ctagcctagc cagcgggggac 120

cggatccgga ggggtggagcg gccaggtgag ccctgaaagg tggggcgggg cgggggcgct 180
 ctgggccccca ccccgggatc tggtgacgcc ggggctggaa ttgacaccg gacggcggcg 240
 ggcaggaggc tgctgaggga tggagtggg ctcggcccc agatgcggcc cgcgggctct 300
 gccagcaaca agtcctcgg gccccagccc tcgtgcgac tggggcttgg agccctgcac 360
 ccaagggcac agaccggctg ccaaggcccc actttaact aaaagaggcg ctgccaggtg 420
 cacaactctg ggcatgatcc acttgagctt cgggggaaag cccagcactg gtcccaggag 480
 aggcgcctag aaggacacgg accaggaccc ctttggtatg gagtgaacgc tgagcatgga 540
 gtggaaggaa ctcaagttac tactttctcc aaccacctg gtaccttcag ccctgaagta 600
 cagagcagaa gggctctaga agacaggacc acagctgtgt gagtctcccc cctgaggcct 660
 tagacgatct ctgagctcag ctgagcttg ttgccccatc tggagaagtg agccattgat 720
 tgaccttggt gcctcgcgaa ggaacaggtc ctgccaagca cctaacacag agagcaaggt 780
 tctccatcgc agctaccgct gctgagttga ctctagctac tccaacctcc tgggtcgctt 840
 cgagagactg gagtgggaagg aggaataccc caaaggataa ctaactcacc ttacagtttg 900
 caagctgccg caggaagagg gtggggaaac ggggtccacga aggtctctga tgggagcttc 960
 tggagccgaa agct atg gaa ctg gga ctt gca gag cct act gca ttg tcc 1010
 Met Glu Leu Gly Leu Ala Glu Pro Thr Ala Leu Ser
 1 5 10
 cac tgc ctc cgg cct agg tgg cag tca gcc tgg tgg cca acc cta gct 1058
 His Cys Leu Arg Pro Arg Trp Gln Ser Ala Trp Trp Pro Thr Leu Ala
 15 20 25
 gtt cta gcc ctg ctg agc tgc gtc aca gaa gct tcc ctg gac cca atg 1106
 Val Leu Ala Leu Leu Ser Cys Val Thr Glu Ala Ser Leu Asp Pro Met
 30 35 40
 tcc cgc agc ccc gcc gct cgc gac ggt ccc tca ccg gtc ttg ggc ccc 1154
 Ser Arg Ser Pro Ala Ala Arg Asp Gly Pro Ser Pro Val Leu Ala Pro
 45 50 55 60
 ccc acg gac cac ctg cct ggg gga cac act gcg cat ttg tgc agc gaa 1202
 Pro Thr Asp His Leu Pro Gly Gly His Thr Ala His Leu Cys Ser Glu

65 70 75

aga acc ctg cga ccc ccg cct cag tct cct cag ccc gca ccc ccg ccg 1250
Arg Thr Leu Arg Pro Pro Pro Gln Ser Pro Gln Pro Ala Pro Pro Pro
80 85 90

cct ggt ccc gcg ctc cag tct cct ccc gct gcg ctc cgc ggg gca cgc 1298
Pro Gly Pro Ala Leu Gln Ser Pro Pro Ala Ala Leu Arg Gly Ala Arg
95 100 105

gcg gcg cgt gca gga acc cgg agc agc cgc gca cgg acc aca gat gcg 1346
Ala Ala Arg Ala Gly Thr Arg Ser Ser Arg Ala Arg Thr Thr Asp Ala
110 115 120

cgc ggc tgc cgc ctg cgc tcg cag ctg gtg ccg gtg agc gcg ctc ggc 1394
Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val Ser Ala Leu Gly
125 130 135 140

cta ggc cac agc tcc gac gag ctg ata cgt ttc cgc ttc tgc agc ggc 1442
Leu Gly His Ser Ser Asp Glu Leu Ile Arg Phe Arg Phe Cys Ser Gly
145 150 155

tcg tgc cgc cga gca cgc tcc cag cac gat ctc agt ctg gcc agc cta 1490
Ser Cys Arg Arg Ala Arg Ser Gln His Asp Leu Ser Leu Ala Ser Leu
160 165 170

ctg ggc gct ggg gcc cta cgg tcg cct ccc ggg tcc cgg ccg atc agc 1538
Leu Gly Ala Gly Ala Leu Arg Ser Pro Pro Gly Ser Arg Pro Ile Ser
175 180 185

cag ccc tgc tgc cgg ccc act cgc tat gag gcc gtc tcc ttc atg gac 1586
Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp
190 195 200

gtg aac agc acc tgg agg acc gtg gac cac ctc tcc gcc act gcc tgc 1634
Val Asn Ser Thr Trp Arg Thr Val Asp His Leu Ser Ala Thr Ala Cys
205 210 215 220

ggc tgt ctg ggc tgaggatgat ctatctccaa gcctttgcac actagacca 1686
Gly Cys Leu Gly

tgtgttgecc tacctggaac agtccaccg ggctcacta accaggagcc tcaactcagc 1746

aggatatgga ggctgcagag ctcaggcccc aggccggtga gtgacagacg tcgtcggcat 1806

gacagacaga gtgaaagatg tcggaaccac tgaccaacag tccaagtgtg ttcattggatc 1866

ccagctctac agacaggaga aacctcagct aaagagaact cctctgggag aatccagaaa 1926

tggccctctg tcttggggaa tgaatttga agagatatat atacatatat acattgtagt 1986

cgcggtgctg gaccagcctg tgctgaaacc agtcccgtgt tcacttgtgg aagccgaagc 2046

cctatttatt atttctaaat tattttatta ctttgaaaaa aaacgggcaa gtcggcctcc 2106

ctttagtgag ggtaatttg tgatcccggg 2136

<210> 16

<211> 224

<212> PRT

<213> Murinae gen. sp.

<400> 16

Met Glu Leu Gly Leu Ala Glu Pro Thr Ala Leu Ser His Cys Leu Arg

1 5 10 15

Pro Arg Trp Gln Ser Ala Trp Trp Pro Thr Leu Ala Val Leu Ala Leu

20 25 30

Leu Ser Cys Val Thr Glu Ala Ser Leu Asp Pro Met Ser Arg Ser Pro

35 40 45

Ala Ala Arg Asp Gly Pro Ser Pro Val Leu Ala Pro Pro Thr Asp His

50 55 60

Leu Pro Gly Gly His Thr Ala His Leu Cys Ser Glu Arg Thr Leu Arg

65 70 75 80

Pro Pro Pro Gln Ser Pro Gln Pro Ala Pro Pro Pro Pro Gly Pro Ala

85 90 95

Leu Gln Ser Pro Pro Ala Ala Leu Arg Gly Ala Arg Ala Ala Arg Ala

100 105 110

Gly Thr Arg Ser Ser Arg Ala Arg Thr Thr Asp Ala Arg Gly Cys Arg

115 120 125

Leu Arg Ser Gln Leu Val Pro Val Ser Ala Leu Gly Leu Gly His Ser

130 135 140

Ser Asp Glu Leu Ile Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg

145	150	155	160
Ala Arg Ser Gln His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly			
165	170	175	
Ala Leu Arg Ser Pro Pro Gly Ser Arg Pro Ile Ser Gln Pro Cys Cys			
180	185	190	
Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr			
195	200	205	
Trp Arg Thr Val Asp His Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly			
210	215	220	

<210> 17
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR Primer

<400> 17	
cctggccagc ctactggg	18

<210> 18
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR Primer

<400> 18	
aaggagaccg cttcgtagcg	20

<210> 19
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 19

atggaacttg gacttg

17

<210> 20

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 20

tccatcacc accggc

16

<210> 21

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 21

ggccaccgct ccgacgag

18

<210> 22

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 22

ggcgggtccac ggttctccag

20

<210> 23

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 23

ccaagccac ctgggtgcc tcttctcc 29

<210> 24

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 24

catcaccac cggcaggggc ctctcag 27

<210> 25

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 25

gagcccatgc ccggcctgat ctcagcccga ggaca 35

<210> 26

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 26

ccctggctga ggccgctggc tagtgggact ctgc 34

<210> 27

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hybridization
Probe

<220>

<221> misc_feature

<222> (1)

<223> Wherein n is designated as a, c, t or g

<400> 27

ncaggtggtc cgtggggggc gccagaccg g 31

<210> 28

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 28

ctaggagccc atgccc 16

<210> 29

<211> 351

<212> DNA

<213> Homo sapiens

<400> 29

atggctggag gaccgggac tcgtgctcgt gcagcaggag cacgtggctg tcgtctgcgt 60
tctcaactag tgccgggtcg tgcactcgga ctgggacacc gttccgacga actagtacgt 120
tttcgtttt gttcaggatc ttgtcgtcgt gcacgttctc cgcattgatc atctctagca 180
tctctactag gagecgggag actaagaccg ccgccgggat ctgacctgt atctcaacct 240
tgtttagac ctactagata cgaagcagta tcttcatgg acgtaaactc tacatggaga 300
accgtagata gactatctgc aaccgcatgt ggctgtctag gatgataata g 351

<210> 30

<211> 414

<212> DNA

<213> Homo sapiens

<400> 30

atgggccatc atcatcatca tcacatcat catcactcga gcggccatat cgacgacgac 60
gacaaggetg gaggaccggg atctcgtgct cgtgcagcag gacacgtgg ctgtcgtctg 120
cgttctcaac tagtgccggg gcgtgcactc ggactgggac accgttccga cgaactagta 180
cgtttctgtt ttgttcagg atctgtcgt cgtgcacgtt ctccgcatga tctatctcta 240
gcattcttac taggagccgg agcactaaga ccgccgccgg gatctagacc tgtatctcaa 300
ccttgttgta gacctactag atacgaagca gtatcttca tggacgtaaa ctctacatgg 360
agaaccgtag atagactatc tgcaaccgca tgtggctgtc taggatgata atag 414

<210> 31

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 31

aaggaaaaaa gcggccgcca tggaactgg acttggagg 39

<210> 32

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 32

tttttcctt ggccggccgt cagcccaggc agccgcagg 39

<210> 33

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 33

gagcgagccc tcagcc 16

<210> 34
<211> 197
<212> PRT
<213> Homo sapiens

<400> 34
Met Gln Arg Trp Lys Ala Ala Ala Leu Ala Ser Val Leu Cys Ser Ser
1 5 10 15

Val Leu Ser Ile Trp Met Cys Arg Glu Gly Leu Leu Leu Ser His Arg
20 25 30

Leu Gly Pro Ala Leu Val Pro Leu His Arg Leu Pro Arg Thr Leu Asp
35 40 45

Ala Arg Ile Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala
50 55 60

Pro Asp Ala Met Glu Leu Arg Glu Leu Thr Pro Trp Ala Gly Arg Pro
65 70 75 80

Pro Gly Pro Arg Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg Ala
85 90 95

Arg Leu Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg Val
100 105 110

Ser Glu Leu Gly Leu Gly Tyr Ala Ser Asp Glu Thr Val Leu Phe Arg
115 120 125

Tyr Cys Ala Gly Ala Cys Glu Ala Ala Ala Arg Val Tyr Asp Leu Gly
130 135 140

Leu Arg Arg Leu Arg Gln Arg Arg Arg Leu Arg Arg Glu Arg Val Arg
145 150 155 160

Ala Gln Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe
165 170 175

Leu Asp Ala His Ser Arg Tyr His Thr Val His Glu Leu Ser Ala Arg
180 185 190

Glu Cys Ala Cys Val
195

<210> 35
<211> 220
<212> PRT
<213> Homo sapiens

<400> 35
Met Glu Leu Gly Leu Gly Gly Leu Ser Thr Leu Ser His Cys Pro Trp
1 5 10 15

Pro Arg Arg Gln Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala Leu
20 25 30

Leu Ser Ser Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser Pro
35 40 45

Ala Pro Arg Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly His
50 55 60

Leu Pro Gly Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg
65 70 75 80

Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Ala Pro Pro
85 90 95

Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly Gly Pro Gly
100 105 110

Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln
115 120 125

Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu
130 135 140

Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro
145 150 155 160

His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro
165 170 175

Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg
180 185 190

Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val
195 200 205

Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly
210 215 220

<210> 36

<211> 156

<212> PRT

<213> Homo sapiens

<400> 36

Met Ala Val Gly Lys Phe Leu Leu Gly Ser Leu Leu Leu Ser Leu
1 5 10 15

Gln Leu Gly Gln Gly Trp Gly Pro Asp Ala Arg Gly Val Pro Val Ala
20 25 30

Asp Gly Glu Phe Ser Ser Glu Gln Val Ala Lys Ala Gly Gly Thr Trp
35 40 45

Leu Gly Thr His Arg Pro Leu Ala Arg Leu Arg Arg Ala Leu Ser Gly
50 55 60

Pro Cys Gln Leu Trp Ser Leu Thr Leu Ser Val Ala Glu Leu Gly Leu
65 70 75 80

Gly Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr Cys Ala Gly Ser
85 90 95

Cys Pro Arg Gly Ala Arg Thr Gln His Gly Leu Ala Leu Ala Arg Leu
100 105 110

Gln Gly Gln Gly Arg Ala His Gly Gly Pro Cys Cys Arg Pro Thr Arg
115 120 125

Tyr Thr Asp Val Ala Phe Leu Asp Asp Arg His Arg Trp Gln Arg Leu
130 135 140

Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
145 150 155

<210> 37

<211> 211

<212> PRT

<213> Homo sapiens

<400> 37

Met Lys Leu Trp Asp Val Val Ala Val Cys Leu Val Leu Leu His Thr
1 5 10 15

Ala Ser Ala Phe Pro Leu Pro Ala Gly Lys Arg Pro Pro Glu Ala Pro
20 25 30

Ala Glu Asp Arg Ser Leu Gly Arg Arg Arg Ala Pro Phe Ala Leu Ser
35 40 45

Ser Asp Ser Asn Met Pro Glu Asp Tyr Pro Asp Gln Phe Asp Asp Val
50 55 60

Met Asp Phe Ile Gln Ala Thr Ile Lys Arg Leu Lys Arg Ser Pro Asp
65 70 75 80

Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala
85 90 95

Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg
100 105 110

Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn Val Thr
115 120 125

Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr
130 135 140

Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu
145 150 155 160

Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Ser Asp Lys Val Gly Gln
165 170 175

Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp
180 185 190

Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys Arg Cys
195 200 205

Gly Cys Ile
210

<210> 38

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 38

gctggcccgg ctgcaggg 18

<210> 39

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 39

gctgcgacga ctgcgcca 18

<210> 40

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 40

attgaaaaac ttatccag 18

<210> 41

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 41

taggccacgt cggtagcg 20

<210> 42
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 42
aaggacacct cgtcctcgta ggc 23

<210> 43
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 43
aacgacaggt catcatcaaa ggc 23

<210> 44
<211> 14
<212> PRT
<213> artificial

<220>
<223> amino acids 30-43 of SEQ ID NO:9

<400> 44

Gly Pro Gly Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys
1 5 10

<210> 45
<211> 14
<212> PRT
<213> artificial

<220>
<223> amino acids 57-70 of SEQ ID NO:9

<400> 45

Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys
1 5 10

<210> 46

<211> 12

<212> PRT

<213> artificial

<220>

<223> amino acids 74-85 of SEQ ID NO: 9

<400> 46

Cys Arg Arg Ala Arg Ser Pro His Asp Leu Ser Leu
1 5 10

<210> 47

<211> 14

<212> PRT

<213> artificial

<220>

<223> amino acids 94-107 of SEQ ID NO: 9

<400> 47

Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys
1 5 10

<210> 48

<211> 14

<212> PRT

<213> artificial

<220>

<223> amino acids 123-136 of SEQ ID NO:9

<400> 48

Ser Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Thr Ala Cys
1 5 10

<210> 49
<211> 211
<212> PRT
<213> homo sapiens

<400> 49

Met Lys Leu Trp Asp Val Val Ala Val Cys Leu Val Leu Leu His Thr
1 5 10 15

Ala Ser Ala Phe Pro Leu Pro Ala Gly Lys Arg Pro Pro Glu Ala Pro
20 25 30

Ala Glu Asp Arg Ser Leu Gly Arg Arg Arg Ala Pro Phe Ala Leu Ser
35 40 45

Ser Asp Ser Asn Met Pro Glu Asp Tyr Pro Asp Gln Phe Asp Asp Val
50 55 60

Met Asp Phe Ile Gln Ala Thr Ile Lys Arg Leu Lys Arg Ser Pro Asp
65 70 75 80

Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala
85 90 95

Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg
100 105 110

Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn Val Thr
115 120 125

Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr
130 135 140

Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu

145 150 155 160

Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Ser Asp Lys Val Gly Gln
 165 170 175

Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp
 180 185 190

Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys Arg Cys
 195 200 205

Gly Cys Ile
 210

<210> 50

<211> 156

<212> PRT

<213> Homo sapiens

<400> 50

Met Ala Val Gly Lys Phe Leu Leu Gly Ser Leu Leu Leu Leu Ser Leu
1 5 10 15

Gln Leu Gly Gln Gly Trp Gly Pro Asp Ala Arg Gly Val Pro Val Ala
 20 25 30

Asp Gly Glu Phe Ser Ser Glu Gln Val Ala Lys Ala Gly Gly Thr Trp
 35 40 45

Leu Gly Thr His Arg Pro Leu Ala Arg Leu Arg Arg Ala Leu Ser Gly
 50 55 60

Pro Cys Gln Leu Trp Ser Leu Thr Leu Ser Val Ala Glu Leu Gly Leu
65 70 75 80

Gly Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr Cys Ala Gly Ser
85 90 95

Cys Pro Arg Gly Ala Arg Thr Gln His Gly Leu Ala Leu Ala Arg Leu
100 105 110

Gln Gly Gln Gly Arg Ala His Gly Gly Pro Cys Cys Arg Pro Thr Arg
115 120 125

Tyr Thr Asp Val Ala Phe Leu Asp Asp Arg His Arg Trp Gln Arg Leu
130 135 140

Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
145 150 155

<210> 51

<211> 197

<212> PRT

<213> homo sapiens

<400> 51

Met Gln Arg Trp Lys Ala Ala Ala Leu Ala Ser Val Leu Cys Ser Ser
1 5 10 15

Val Leu Ser Ile Trp Met Cys Arg Glu Gly Leu Leu Leu Ser His Arg
20 25 30

Leu Gly Pro Ala Leu Val Pro Leu His Arg Leu Pro Arg Thr Leu Asp
35 40 45

Ala Arg Ile Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala
50 55 60

Pro Asp Ala Met Glu Leu Arg Glu Leu Thr Pro Trp Ala Gly Arg Pro
65 70 75 80

Pro Gly Pro Arg Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg Ala
85 90 95

Arg Leu Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg Val
100 105 110

Ser Glu Leu Gly Leu Gly Tyr Ala Ser Asp Glu Thr Val Leu Phe Arg
115 120 125

Tyr Cys Ala Gly Ala Cys Glu Ala Ala Ala Arg Val Tyr Asp Leu Gly
130 135 140

Leu Arg Arg Leu Arg Gln Arg Arg Arg Leu Arg Arg Glu Arg Val Arg
145 150 155 160

Ala Gln Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe
165 170 175

Leu Asp Ala His Ser Arg Tyr His Thr Val His Glu Leu Ser Ala Arg
180 185 190

Glu Cys Ala Cys Val
195

<210> 52

<211> 4

<212> PRT

<213> artificial

<220>

<223> amino acid fragment

<400> 52

Asn Glu Gln Lys

1

<210> 53
<211> 4
<212> PRT
<213> artificial

<220>
<223> amino acid fragment

<400> 53

Asn His Gln Lys
1

<210> 54
<211> 4
<212> PRT
<213> artificial

<220>
<223> amino acid fragment

<400> 54

Asn Asp Glu Gln
1

<210> 55
<211> 4
<212> PRT
<213> artificial

<220>
<223> amino acid fragment

<400> 55

Gln His Arg Lys
1

<210> 56
<211> 4
<212> PRT

<213> artificial

<220>

<223> amino acid fragment

<400> 56

Met Ile Leu Val

1

<210> 57

<211> 4

<212> PRT

<213> artificial

<220>

<223> amino acid fragment

<400> 57

Met Ile Leu Phe

1

<210> 58

<211> 4

<212> PRT

<213> artificial

<220>

<223> amino acid fragment

<400> 58

Ser Thr Asn Lys

1

<210> 59

<211> 4

<212> PRT

<213> artificial

<220>

<223> amino acid fragment

<400> 59

Ser Thr Pro Ala

1

<210> 60

<211> 4

<212> PRT

<213> artificial

<220>

<223> amino acid fragment

<400> 60

Ser Gly Asn Asp

1

<210> 61

<211> 6

<212> PRT

<213> artificial

<220>

<223> amino acid fragment

<400> 61

Ser Asn Asp Glu Gln Lys

1

5

<210> 62

<211> 6

<212> PRT

<213> artificial

<220>

<223> amino acid fragment

<400> 62

Asn Asp Glu Gln His Lys

1 5

<210> 63

<211> 6

<212> PRT

<213> artificial

<220>

<223> amino acid fragment

<400> 63

Asn Glu Gln His Arg Lys

1 5

<210> 64

<211> 4

<212> PRT

<213> artificial

<220>

<223> amino acid fragment

<400> 64

Val Leu Ile Met

1

<210> 65

<211> 4

<212> PRT

<213> artificial

<220>

<223> amino acid fragment (GDNF subfamily fingerprint)

<400> 65

Leu Gly Leu Gly

1

<210> 66

<211> 8
<212> PRT
<213> artificial

<220>
<223> amino acid fragment (GDNF subfamily fingerprint)

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Wherein the amino acid at position 3 is Y (Tyrosine) or F (Phenylalanine).

<400> 66

Phe Arg Xaa Cys Ser Gly Ser Cys
1 5

<210> 67
<211> 6
<212> PRT
<213> artificial

<220>
<223> amino acid fragment (GDNF subfamily fingerprint)

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Wherein the amino acid at position 2 can be any amino acid.

<400> 67

Gln Xaa Cys Cys Arg Pro
1 5

<210> 68
<211> 7
<212> PRT
<213> artificial

<220>
<223> amino acid fragment (GDNF subfamily fingerpring)

<220>
<221> MISC_FEATURE
<222> (3)..(4)
<223> Wherein amino acids at positions 3-4 can be any amino acid.

<400> 68

Ser Ala Xaa Xaa Cys Gly Cys
1 5

<210> 69
<211> 18
<212> DNA
<213> artificial

<220>
<223> nucleotide fragment of persephin

<400> 69
cctggccagc ctactggg 18

<210> 70
<211> 18
<212> DNA
<213> artificial

<220>
<223> nucleotide fragment of neurturin

<400> 70
gctggcccgg ctgcaggg 18

<210> 71
<211> 18
<212> DNA
<213> artificial

<220>
<223> nucleotide fragment of GDNF

<400> 71

attgaaaaac ttatccag 18

<210> 72

<211> 20

<212> DNA

<213> artificial

<220>

<223> nucleotide fragment of persephin

<400> 72

taggccacgt cggtagcg 20

<210> 73

<211> 23

<212> DNA

<213> artificial

<220>

<223> nucleotide fragment of neurturin

<400> 73

aaggacacct cgtcctcgta ggc 23

<210> 74

<211> 23

<212> DNA

<213> artificial

<220>

<223> nucleotide fragment of GDNF

<400> 74

aacgacaggt catcatcaaa ggc 23

<210> 75

<211> 114

<212> PRT

<213> artificial

<220>

<223> amino acid sequence of neublastin syngene

<400> 75

Met Ala Gly Gly Pro Gly Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly
1 5 10 15

Cys Arg Leu Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly
 20 25 30

His Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys
 35 40 45

Arg Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly
 50 55 60

Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro
65 70 75 80

Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn
 85 90 95

Ser Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys
 100 105 110

Leu Gly

<210> 76

<211> 136

<212> PRT

<213> artificial

<220>

<223> amino acid sequence of hisneublastin syngene

<400> 76

Met Gly His His His His His His His His His Ser Ser Gly His

1 5 10 15

Ile Asp Asp Asp Asp Lys Ala Gly Gly Pro Gly Ser Arg Ala Arg Ala
 20 25 30

Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val Arg
 35 40 45

Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg Phe
 50 55 60

Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro His Asp Leu Ser Leu
65 70 75 80

Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg
 85 90 95

Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser
 100 105 110

Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Leu Ser
 115 120 125

Ala Thr Ala Cys Gly Cys Leu Gly
 130 135